Package 'RbcBook1'

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Title Support for Springer monograph on Bioconductor

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Description tools for building book

Depends R (>= 2.10), Biobase, graph, rpart

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URL http://www.biostat.harvard.edu/~carey

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Contents

bcr.cor *Illustrative datasets for distance measures*

Description

Illustrative datasets for distance measures

Usage

```
data(ALL.dist) # all the components live in here
```

Details

These datasets are used in conjunction with the bioDist package for the distance chapter of the monograph

Value

these are `dist` objects

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(ALL.dist)
objects()
dim(as.matrix(bcr.cor))
```

bcStangle *A function to extract the code chunks from the book for the online supplement*

Description

A function to extract the code chunks from the book for the online supplement.

Usage

```
bcStangle(files = .RbcBook1Files(), outfile= "bioCSpringer.R")
tangleToSingleFiles()
```

Arguments

`files`	character vector with filenames of book chapters. Must have extension `.Rnw`
`outfile`	character of length 1 with the name of the output file.

Details

It should suffice to change to the book's top level directory (e.g. .../Springer1/trunk/Book1) and run `bcStangle()`.

This function is specialized to its one purpose given in the title. It is not envisaged that it could be useful beyond, or even replace Stangle.

`tangleToSingleFiles` creates a directory named Rfiles and tangles each chapter separately into this directory. You must have the current working directory set to the top level directory of the book (Springer/Book1).

Value

Function is called for its side effects.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

See Also

.RbcBook1Files, Stangle

Examples

```
## bcStangle()
```

---

bcSweave *Wrapper for Sweave*

Description

Wrapper for Sweave - allows to set options, or perform additional preprocessing or QC steps.

Usage

```
bcSweave(f)
```

Arguments

`f`	character, filename. Must have extension `.Rnw`

Details

No details.

Value

Function is called for its side effects.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
## bcSweave("Intro.Rnw")
```

---

checkingBookSources *Formatting and standardization checks on book chapters*

Description

Formatting and standardization checks on book chapters

Usage

```
checkVerbatim(files = .RbcBook1Files(ext=".tex"),
              maxc = 70,
             which = "both",
           verbose = TRUE)

checkRnw(files = .RbcBook1Files(),
       verbose = TRUE, stopOnError=FALSE)

checkPackage(files = .RbcBook1Files(ext=".Rnw"),
          verbose = TRUE)

.RbcBook1Files(ext=".Rnw")
```

Arguments

files	character vector with names (and path) of chapter source files
ext	character of length 1. File name extension. .Rnw (the default) and .tex should be the most important cases.
maxc	integer of length 1. Maximal number of characters in a verbatim line. All lines exceeding this limit will be reported in the return value of this function.
which	character of length 1. 'Sinput' will look at Sinput environments, 'Soutput' at Soutput environments, 'both' at both.
verbose	Logical.
stopOnError	Logical. If FALSE, first error found will lead to stop. If TRUE, try to continue checking.

Details

checkVerbatimLines sees whether all verbatim lines have length at most maxc.

checkPackage finds all the occurences of \Rpackage{...} in the text, checks whether the package is known, and returns a named list will all occurences of the packages.

Value

For checkVerbatimLines and checkSetup, a data frame with one row for each offending line and various columns describing it.

For .RbcBook1Files, a character vector.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
f = tempfile()
zap = function(n) paste(formatC(1:n, width=2), collapse=" ")
writeLines(c("*begin{Sinput}", zap(20), zap(30), "*end{Sinput}"), con=f)
checkVerbatim(files=f)
```

---

imageSize *File info for all image files in the book*

Description

File info for all image files in the book

Usage

```
imageSize(dirs= c("Preproc","Analysis","Metadata","Graphs","CaseStudies"), ext=c("pdf", "png"))
```

Arguments

dirs	character vector with directories.
ext	character vector with file name extensions.

Details

No details.

Value

Data frame.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
# a = imageSize()
# print(a[1:10,c(1,4)])
```

perf — *Results of tedious computations for computational inference*

Description

Results of tedious computations for computational inference

Usage

```
data(Survperformance)
```

Details

These datasets are used in conjunction with the computational inference chapter of the monograph

Value

these are `data.frame` objects

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(Survperformance)
objects()
dim(performance)
```

require.RbcBook1 — *Load a lengthy list of packages that are used in the Book*

Description

Load a lengthy list of packages that are used in the Book

Usage

```
require.RbcBook1()
.RbcBook1.pkgs()
```

Details

`require.RbcBook1` can be used to see at once whether all packages required for the book can be loaded.

To do for `.RbcBook1.pkgs`: version numbers?

Value

`.RbcBook1.pkgs` returns a character vector with the names of all packages used in the book.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
## Not run:
library(reposTools)
install.packages2(.RbcBook1.pkgs(), develOK=TRUE)
require.RbcBook1()

## End(Not run)
```

`rpart2gNEL` *rpart to graphNEL Converter*

Description

Creates an object of class `graphNEL` from one of class `rpart`.

Usage

```
rpart2gNEL(tr, remap=function(x) x, nsep="\n")
```

Arguments

`tr`	instance of `rpart` class from `rpart` package.
`remap`	function that maps node names in tree to node names in graph.
`nsep`	token that separates node name and vote tally in the rendering.

Details

Not explicitly used in the book, but the basis for a certain graph illustrating application of rpart. The newer coin/party packages have more interesting rendering approaches based on graphviz.

`grabSplitV` is a utility function for acquiring the variable names, `remapAff` will remap affymetrix probe names to gene symbols for use in the `remap` parameter.

Value

a `graphNEL-class` instance with nodes constructed to convey information on the data tree fit

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

See Also

`rpart`, `graphNEL-class`

Examples

```
library(rpart)
example(rpart)
ff = rpart2gNEL(fit2)
ff
nodes(ff)
```

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